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<120> L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS  
  
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<151> 2003-11-27  
  
<150> DE 102 56 381.0  
<151> 2002-12-02  
  
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 tcaggaaatg cgggtggcgtt cacatcacca caatttcggcgtt aattgtgttgc acatcgttgc 180  
 tcgttgc ttcggcgtt ttcggcgtt ttcggcgtt ttcggcgtt ttcggcgtt 240  
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 acatt 125

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 ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct 96  
 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala  
   20               25               30  
 cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc 144  
 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr  
   35               40               45

tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg	192
Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp	
50 55 60	
tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac	240
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp	
65 70 75 80	
agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att	288
Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile	
85 90 95	
ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg	336
Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu	
100 105 110	
ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc	384
Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg	
115 120 125	
aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat	432
Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr	
130 135 140	
gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct	480
Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala	
145 150 155 160	
cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac	528
Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr	
165 170 175	
tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta	576
Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu	
180 185 190	
tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc	624
Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala	
195 200 205	
tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc	672
Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser	
210 215 220	
agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac	720
Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His	
225 230 235 240	
aac gcc ccc ttg ctg aaa gtg ggc ggc agt tcc atg att ttt gcg	768
Asn Ala Pro Leu Leu Lys Val Gly Gly Ser Ser Met Ile Phe Ala	
245 250 255	
cgc gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc	816
Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly	
260 265 270	
ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa ggc	864
Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala	
275 280 285	
atc aat gac ccc gta ggc cac tat tcc aaa ccc gag gcc acc cgt ctg	912
Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu	
290 295 300	
gtg ctg gac ttg ggg cac cga gac ccc atg act cgg gtg cac tcc aaa	960
Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys	
305 310 315 320	
agc gtg acc agg gaa gag gct ccc gag caa ggt gtg caa agc aag att	1008
Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile	
325 330 335	
gcc tca gtc gct atc agc cat cca cag gac tcg gac aca ctg cta gtg	1056
Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val	
340 345 350	

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 Gln Glu Pro Ser  
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1071

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 35 40 45  
 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp  
 50 55 60  
 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp  
 65 70 75 80  
 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile  
 85 90 95  
 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu  
 100 105 110  
 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg  
 115 120 125  
 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr  
 130 135 140  
 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala  
 145 150 155 160  
 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr  
 165 170 175  
 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu  
 180 185 190  
 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala  
 195 200 205  
 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser  
 210 215 220  
 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His  
 225 230 235 240  
 Asn Ala Pro Leu Leu Lys Val Gly Gly Ser Ser Met Ile Phe Ala  
 245 250 255  
 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly  
 260 265 270  
 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala  
 275 280 285  
 Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu  
 290 295 300  
 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys  
 305 310 315 320  
 Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile  
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 Gln Glu Pro Ser  
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gcg gcg gtg ggg att gat gtc gag gag gcg ctg cgc caa ctt gat cgt	96
Ala Ala Val Gly Ile Asp Val Glu Ala Leu Arg Gln Leu Asp Arg	
20                  25                  30	
tta ccc gtt tca atg cac tgc tgg cag ggc gat gat gtt tcc ggt ttt	144
Leu Pro Val Ser Met His Cys Trp Gln Gly Asp Asp Val Ser Gly Phe	
35                  40                  45	
gaa aac ccg gaa ggt tcg ctg acc ggg ggg att cag gcc aca ggc aat	192
Glu Asn Pro Glu Gly Ser Leu Thr Gly Gly Ile Gln Ala Thr Gly Asn	
50                  55                  60	
tat ccg ggc aaa gcg cgt aat gcc agt gag cta cgt gcc gat ctg gaa	240
Tyr Pro Gly Lys Ala Arg Asn Ala Ser Glu Leu Arg Ala Asp Leu Glu	
65                  70                  75                  80	
cag gct atg cgg ctg att ccg ggg ccg aaa cgg ctt aat tta cat gcc	288
Gln Ala Met Arg Leu Ile Pro Gly Pro Lys Arg Leu Asn Leu His Ala	
85                  90                  95	
atc tat ctg gaa tca gat acg cca gtc tcg cgc gac cag atc aaa cca	336
Ile Tyr Leu Glu Ser Asp Thr Pro Val Ser Arg Asp Gln Ile Lys Pro	
100                105                110	
gag cac ttc aaa aac tgg gtt gaa tgg gcg aaa gcc aat cag ctc ggt	384
Glu His Phe Lys Asn Trp Val Glu Trp Ala Lys Ala Asn Gln Leu Gly	
115                120                125	
ctg gat ttt aac ccc tcc tgc ttt tcg cat ccg cta agc gcc gat ggc	432
Leu Asp Phe Asn Pro Ser Cys Phe Ser His Pro Leu Ser Ala Asp Gly	
130                135                140	
ttt acg ctt tcc cat gcc gac gac att cgc cag ttc tgg att gat	480
Phe Thr Leu Ser His Ala Asp Asp Ser Ile Arg Gln Phe Trp Ile Asp	
145                150                155                160	
cac tgc aaa gcc agc cgt cgc gtt tcg gcc tat ttt ggc gag caa ctc	528
His Cys Lys Ala Ser Arg Arg Val Ser Ala Tyr Phe Gly Glu Gln Leu	
165                170                175	
ggc aca cca tcg gtg atg aac atc tgg atc ccg gat ggt atg aaa gat	576
Gly Thr Pro Ser Val Met Asn Ile Trp Ile Pro Asp Gly Met Lys Asp	
180                185                190	
atc acc gtt gac cgt ctc gcc ccg cgt cag cgt ctg ctg gca gca ctg	624
Ile Thr Val Asp Arg Leu Ala Pro Arg Gln Arg Leu Leu Ala Ala Leu	
195                200                205	
gat gag gtg atc agc gag aag cta aac cct gcg cac cat atc gac gcc	672
Asp Glu Val Ile Ser Glu Lys Leu Asn Pro Ala His His Ile Asp Ala	
210                215                220	
gtt gag agc aaa ttg ttt ggc att ggc gca gag agc tac acg gtt ggc	720
Val Glu Ser Lys Leu Phe Gly Ile Gly Ala Glu Ser Tyr Thr Val Gly	
225                230                235                240	
tcc aat gag ttt tac atg ggg tat gcc acc agc cgc cag act gcg ctg	768
Ser Asn Glu Phe Tyr Met Gly Tyr Ala Thr Ser Arg Gln Thr Ala Leu	

245	250	255	
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Cys Leu Asp Ala Gly His Phe His Pro Thr Glu Val Ile Ser Asp Lys			
260	265	270	
att tcc gcc gcc atg ctg tat gtg ccg cag ttg ctg ctg cac gtc agc			864
Ile Ser Ala Ala Met Leu Tyr Val Pro Gln Leu Leu Leu His Val Ser			
275	280	285	
cgt ccg gtt cgc tgg gac agc gat cac gta gtg ctg ctg gat gat gaa			912
Arg Pro Val Arg Trp Asp Ser Asp His Val Val Leu Leu Asp Asp Glu			
290	295	300	
acc cag gca att gcc agt gag att gtg cgt cac gat ctg ttt gac cgg			960
Thr Gln Ala Ile Ala Ser Glu Ile Val Arg His Asp Leu Phe Asp Arg			
305	310	315	320
gtg cat atc ggc ctt gac ttc ttc gat gcc tct atc aac cgc att gcc			1008
Val His Ile Gly Leu Asp Phe Phe Asp Ala Ser Ile Asn Arg Ile Ala			
325	330	335	
gcg tgg gtc att ggt aca cgc aat atg aaa aaa gcc ctg ctg cgt gcg			1056
Ala Trp Val Ile Gly Thr Arg Asn Met Lys Lys Ala Leu Leu Arg Ala			
340	345	350	
ttg ctg gaa cct acc gct gac gtg cgc aag ctg gaa gcg gcg ggc gat			1104
Leu Leu Glu Pro Thr Ala Asp Val Arg Lys Leu Glu Ala Ala Gly Asp			
355	360	365	
tac act gcg cgt ctg gca ctg ctg gaa gag cag aaa tcg ttg ccg tgg			1152
Tyr Thr Ala Arg Leu Ala Leu Glu Glu Gln Lys Ser Leu Pro Trp			
370	375	380	
cag gcg gtc tgg gaa atg tat tgc caa cgt cac gat acg cca gca ggt			1200
Gln Ala Val Trp Glu Met Tyr Cys Gln Arg His Asp Thr Pro Ala Gly			
385	390	395	400
agc gaa tgg ctg gag agc gtg cgg gct tat gag aaa gaa att ttg agt			1248
Ser Glu Trp Leu Glu Ser Val Arg Ala Tyr Glu Lys Glu Ile Leu Ser			
405	410	415	
cgc cgc ggg taa			1260
Arg Arg Gly			

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&lt;212&gt; PRT

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Glu Asn Pro Glu Gly Ser Leu Thr Gly Gly Ile Gln Ala Thr Gly Asn			
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Tyr Pro Gly Lys Ala Arg Asn Ala Ser Glu Leu Arg Ala Asp Leu Glu			
65	70	75	80
Gln Ala Met Arg Leu Ile Pro Gly Pro Lys Arg Leu Asn Leu His Ala			
85	90	95	
Ile Tyr Leu Glu Ser Asp Thr Pro Val Ser Arg Asp Gln Ile Lys Pro			
100	105	110	
Glu His Phe Lys Asn Trp Val Glu Trp Ala Lys Ala Asn Gln Leu Gly			
115	120	125	
Leu Asp Phe Asn Pro Ser Cys Phe Ser His Pro Leu Ser Ala Asp Gly			

130	135	140
Phe	Thr	Leu Ser His Ala Asp Asp Ser Ile Arg Gln Phe Trp Ile Asp
145	150	155 160
His	Cys Lys Ala Ser Arg Arg Val Ser Ala Tyr Phe Gly Glu Gln Leu	
	165	170 175
Gly	Thr Pro Ser Val Met Asn Ile Trp Ile Pro Asp Gly Met Lys Asp	
	180	185 190
Ile	Thr Val Asp Arg Leu Ala Pro Arg Gln Arg Leu Leu Ala Ala Leu	
	195	200 205
Asp	Glu Val Ile Ser Glu Lys Leu Asn Pro Ala His His Ile Asp Ala	
	210	215 220
Val	Glu Ser Lys Leu Phe Gly Ile Gly Ala Glu Ser Tyr Thr Val Gly	
	225	230 235 240
Ser	Asn Glu Phe Tyr Met Gly Tyr Ala Thr Ser Arg Gln Thr Ala Leu	
	245	250 255
Cys	Leu Asp Ala Gly His Phe His Pro Thr Glu Val Ile Ser Asp Lys	
	260	265 270
Ile	Ser Ala Ala Met Leu Tyr Val Pro Gln Leu Leu Leu His Val Ser	
	275	280 285
Arg	Pro Val Arg Trp Asp Ser Asp His Val Val Leu Leu Asp Asp Glu	
	290	295 300
Thr	Gln Ala Ile Ala Ser Glu Ile Val Arg His Asp Leu Phe Asp Arg	
	305	310 315 320
Val	His Ile Gly Leu Asp Phe Phe Asp Ala Ser Ile Asn Arg Ile Ala	
	325	330 335
Ala	Trp Val Ile Gly Thr Arg Asn Met Lys Lys Ala Leu Leu Arg Ala	
	340	345 350
Leu	Leu Glu Pro Thr Ala Asp Val Arg Lys Leu Glu Ala Ala Gly Asp	
	355	360 365
Tyr	Thr Ala Arg Leu Ala Leu Leu Glu Glu Gln Lys Ser Leu Pro Trp	
	370	375 380
Gln	Ala Val Trp Glu Met Tyr Cys Gln Arg His Asp Thr Pro Ala Gly	
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Arg	Arg Gly	

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1																15
cgc	gtg	atg	ctg	gcg	cgt	tac	gag	cgt	gaa	tgc	cgc	agc	ctg	acg	ctg	96
Arg	Val	Met	Leu	Ala	Arg	Tyr	Glu	Arg	Glu	Cys	Arg	Ser	Leu	Thr	Leu	
																30
cgc	gaa	atc	cat	cgt	ttt	aac	aat	ggg	ctg	cat	agt	cag	aac	ggc	tat	144
Arg	Glu	Ile	His	Arg	Phe	Asn	Asn	Gly	Leu	His	Ser	Gln	Asn	Gly	Tyr	
																35
gtc	acc	tgg	gat	gtg	gat	agc	ctt	gaa	agt	gcc	att	cgc	ctt	gga	tta	192

Val Thr Trp Asp Val Asp Ser Leu Glu Ser Ala Ile Arg Leu Gly Leu			
50	55	60	
aac aag gtg tgc gag gaa ggg att cgt atc gat agc att ggg att gat			240
Asn Lys Val Cys Glu Glu Gly Ile Arg Ile Asp Ser Ile Gly Ile Asp			
65	70	75	80
acc tgg ggc gtg gac ttt gtg ctg ctc gac caa cag ggt cag cgt gtg			288
Thr Trp Gly Val Asp Phe Val Leu Leu Asp Gln Gln Gly Gln Arg Val			
85	90	95	
ggc ctg ccc gtt gct tat cgc gat agc cgc acc aat ggc cta atg gcg			336
Gly Leu Pro Val Ala Tyr Arg Asp Ser Arg Thr Asn Gly Leu Met Ala			
100	105	110	
cag gca caa caa ctc ggc aaa cgc gat att tat caa cgt agc ggc			384
Gln Ala Gln Gln Leu Gly Lys Arg Asp Ile Tyr Gln Arg Ser Gly			
115	120	125	
atc cag ttt ctg ccc ttc aat acg ctt tat cag ttg cgt gcg ctg acg			432
Ile Gln Phe Leu Pro Phe Asn Thr Leu Tyr Gln Leu Arg Ala Leu Thr			
130	135	140	
gag caa caa cct gaa ctt att cca cac att gct cac gct ctg ctg atg			480
Glu Gln Gln Pro Glu Leu Ile Pro His Ile Ala His Ala Leu Leu Met			
145	150	155	160
ccg gat tac ttc agt tat cgc ctg acc ggc aag atg aac tgg gaa tat			528
Pro Asp Tyr Phe Ser Tyr Arg Leu Thr Gly Lys Met Asn Trp Glu Tyr			
165	170	175	
acc aac gcc acg acc acg caa ctg gtc aat atc aat agc gac gac tgg			576
Thr Asn Ala Thr Thr Thr Gln Leu Val Asn Ile Asn Ser Asp Asp Trp			
180	185	190	
gac gag tcg cta ctg gcg tgg agc ggg gcc aac aaa gcc tgg ttt ggt			624
Asp Glu Ser Leu Leu Ala Trp Ser Gly Ala Asn Lys Ala Trp Phe Gly			
195	200	205	
cgc ccg acg cat ccg ggt aat gtc ata ggt cac tgg att tgc ccg cag			672
Arg Pro Thr His Pro Gly Asn Val Ile Gly His Trp Ile Cys Pro Gln			
210	215	220	
ggt aat gag att cca gtg gtc gcc gtt gcc agc cat gat acc gcc agc			720
Gly Asn Glu Ile Pro Val Val Ala Val Ala Ser His Asp Thr Ala Ser			
225	230	235	240
gcg gtt atc gcc tcg ccg tta aac ggc tca cgt gct gct tat ctc tct			768
Ala Val Ile Ala Ser Pro Leu Asn Gly Ser Arg Ala Ala Tyr Leu Ser			
245	250	255	
tct ggc acc tgg tca ttg atg ggc ttc gaa agc cag acg cca ttt acc			816
Ser Gly Thr Trp Ser Leu Met Gly Phe Glu Ser Gln Thr Pro Phe Thr			
260	265	270	
aat gac acg gca ctg gca gcc aac atc acc aat gaa ggc ggg gcg gaa			864
Asn Asp Thr Ala Leu Ala Ala Asn Ile Thr Asn Glu Gly Gly Ala Glu			
275	280	285	
ggt cgc tat cgg gtg ctg aaa aat att atg ggc tta tgg ctg ctt cag			912
Gly Arg Tyr Arg Val Leu Lys Asn Ile Met Gly Leu Trp Leu Leu Gln			
290	295	300	
cga gtg ctt cag gag cag caa atc aac gat ctt ccg gcg ctt atc tcc			960
Arg Val Leu Gln Glu Gln Ile Asn Asp Leu Pro Ala Leu Ile Ser			
305	310	315	320
gcg aca cag gca ctt ccg gct tgc cgc ttc att atc aat ccc aat gac			1008
Ala Thr Gln Ala Leu Pro Ala Cys Arg Phe Ile Ile Asn Pro Asn Asp			
325	330	335	
gat cgc ttt att aat cct gag acg atg tgc agc gaa att cag gct gcg			1056
Asp Arg Phe Ile Asn Pro Glu Thr Met Cys Ser Glu Ile Gln Ala Ala			
340	345	350	
tgt cgg gaa acg gcg caa ccg atc ccg gaa agt gat gct gaa ctg gcg			1104

Cys Arg Glu Thr Ala Gln Pro Ile Pro Glu Ser Asp Ala Glu Leu Ala			
355	360	365	
cgc tgc att ttc gac agt ctg gcg ctg ctg tat gcc gat gtg ttg cat			1152
Arg Cys Ile Phe Asp Ser Leu Ala Leu Leu Tyr Ala Asp Val Leu His			
370	375	380	
gag ctg gcg cag ctg cgc ggt gaa gat ttc tcg caa ctg cat att gtc			1200
Glu Leu Ala Gln Leu Arg Gly Glu Asp Phe Ser Gln Leu His Ile Val			
385	390	395	400
ggc gga ggc tgc cag aac acg ctg ctc aac cag cta tgc gcc gat gcc			1248
Gly Gly Cys Gln Asn Thr Leu Leu Asn Gln Leu Cys Ala Asp Ala			
405	410	415	
tgc ggt att cgg gtg atc gcc ggg cct gtt gaa gcc tcg acg ctc ggc			1296
Cys Gly Ile Arg Val Ile Ala Gly Pro Val Glu Ala Ser Thr Leu Gly			
420	425	430	
aat atc ggc atc cag tta atg acg ctg gat gaa ctc aac aat gtg gat			1344
Asn Ile Gly Ile Gln Leu Met Thr Leu Asp Glu Leu Asn Asn Val Asp			
435	440	445	
gat ttc cgt cag gtc gtc agc acc acc gcg aat ctg acc acc acc ttt acc			1392
Asp Phe Arg Gln Val Val Ser Thr Thr Ala Asn Leu Thr Thr Phe Thr			
450	455	460	
cct aat cct gac agt gaa att gcc cac tat gtg gcg cag att cac tct			1440
Pro Asn Pro Asp Ser Glu Ile Ala His Tyr Val Ala Gln Ile His Ser			
465	470	475	480
aca cga cag aca aag gag ctt tgc gca tga			1470
Thr Arg Gln Thr Lys Glu Leu Cys Ala			
485			

<210> 11			
<211> 489			
<212> PRT			
<213> Escherichia coli			
<400> 11			
Met Thr Phe Arg Asn Cys Val Ala Val Asp Leu Gly Ala Ser Ser Gly			
1	5	10	15
Arg Val Met Leu Ala Arg Tyr Glu Arg Glu Cys Arg Ser Leu Thr Leu			
20	25	30	
Arg Glu Ile His Arg Phe Asn Asn Gly Leu His Ser Gln Asn Gly Tyr			
35	40	45	
Val Thr Trp Asp Val Asp Ser Leu Glu Ser Ala Ile Arg Leu Gly Leu			
50	55	60	
Asn Lys Val Cys Glu Glu Gly Ile Arg Ile Asp Ser Ile Gly Ile Asp			
65	70	75	80
Thr Trp Gly Val Asp Phe Val Leu Leu Asp Gln Gln Gly Gln Arg Val			
85	90	95	
Gly Leu Pro Val Ala Tyr Arg Asp Ser Arg Thr Asn Gly Leu Met Ala			
100	105	110	
Gln Ala Gln Gln Gln Leu Gly Lys Arg Asp Ile Tyr Gln Arg Ser Gly			
115	120	125	
Ile Gln Phe Leu Pro Phe Asn Thr Leu Tyr Gln Leu Arg Ala Leu Thr			
130	135	140	
Glu Gln Gln Pro Glu Leu Ile Pro His Ile Ala His Ala Leu Leu Met			
145	150	155	160
Pro Asp Tyr Phe Ser Tyr Arg Leu Thr Gly Lys Met Asn Trp Glu Tyr			
165	170	175	
Thr Asn Ala Thr Thr Thr Gln Leu Val Asn Ile Asn Ser Asp Asp Trp			
180	185	190	

Asp Glu Ser Leu Leu Ala Trp Ser Gly Ala Asn Lys Ala Trp Phe Gly  
     195                 200                 205  
 Arg Pro Thr His Pro Gly Asn Val Ile Gly His Trp Ile Cys Pro Gln  
     210                 215                 220  
 Gly Asn Glu Ile Pro Val Val Ala Val Ala Ser His Asp Thr Ala Ser  
     225                 230                 235                 240  
 Ala Val Ile Ala Ser Pro Leu Asn Gly Ser Arg Ala Ala Tyr Leu Ser  
     245                 250                 255  
 Ser Gly Thr Trp Ser Leu Met Gly Phe Glu Ser Gln Thr Pro Phe Thr  
     260                 265                 270  
 Asn Asp Thr Ala Leu Ala Ala Asn Ile Thr Asn Glu Gly Gly Ala Glu  
     275                 280                 285  
 Gly Arg Tyr Arg Val Leu Lys Asn Ile Met Gly Leu Trp Leu Leu Gln  
     290                 295                 300  
 Arg Val Leu Gln Glu Gln Gln Ile Asn Asp Leu Pro Ala Leu Ile Ser  
     305                 310                 315                 320  
 Ala Thr Gln Ala Leu Pro Ala Cys Arg Phe Ile Ile Asn Pro Asn Asp  
     325                 330                 335  
 Asp Arg Phe Ile Asn Pro Glu Thr Met Cys Ser Glu Ile Gln Ala Ala  
     340                 345                 350  
 Cys Arg Glu Thr Ala Gln Pro Ile Pro Glu Ser Asp Ala Glu Leu Ala  
     355                 360                 365  
 Arg Cys Ile Phe Asp Ser Leu Ala Leu Leu Tyr Ala Asp Val Leu His  
     370                 375                 380  
 Glu Leu Ala Gln Leu Arg Gly Glu Asp Phe Ser Gln Leu His Ile Val  
     385                 390                 395                 400  
 Gly Gly Cys Gln Asn Thr Leu Leu Asn Gln Leu Cys Ala Asp Ala  
     405                 410                 415  
 Cys Gly Ile Arg Val Ile Ala Gly Pro Val Glu Ala Ser Thr Leu Gly  
     420                 425                 430  
 Asn Ile Gly Ile Gln Leu Met Thr Leu Asp Glu Leu Asn Asn Val Asp  
     435                 440                 445  
 Asp Phe Arg Gln Val Val Ser Thr Thr Ala Asn Leu Thr Thr Phe Thr  
     450                 455                 460  
 Pro Asn Pro Asp Ser Glu Ile Ala His Tyr Val Ala Gln Ile His Ser  
     465                 470                 475                 480  
 Thr Arg Gln Thr Lys Glu Leu Cys Ala  
     485

<210> 12  
 <211> 825  
 <212> DNA  
 <213> Escherichia coli  
 <220>  
 <221> CDS  
 <222> (1)...(822)  
 <223> coding for rhaD (rhamnulose-phosphate aldolase)  
 <400> 12  
 atg caa aac att act cag tcc tgg ttt gtc cag gga atg atc aaa gcc   48  
 Met Gln Asn Ile Thr Gln Ser Trp Phe Val Gln Gly Met Ile Lys Ala  
     1               5               10               15  
 acc acc gac gcc tgg ctg aaa ggc tgg gat gag cgc aac ggc ggc aac   96  
 Thr Thr Asp Ala Trp Leu Lys Gly Trp Asp Glu Arg Asn Gly Gly Asn  
     20               25               30  
 ctg acg cta cgc ctg gat gac gcc gat atc gca cca tat cac gac aat   144  
 Leu Thr Leu Arg Leu Asp Asp Ala Asp Ile Ala Pro Tyr His Asp Asn

35	40	45	
ttc cac caa caa ccg cgc tat atc ccg ctc agc cag ccc atg cct tta			192
Phe His Gln Gln Pro Arg Tyr Ile Pro Leu Ser Gln Pro Met Pro Leu			
50	55	60	
ctg gca aat aca ccg ttt att gtc acc ggc tcg ggc aaa ttc ttc cgt			240
Leu Ala Asn Thr Pro Phe Ile Val Thr Gly Ser Gly Lys Phe Phe Arg			
65	70	75	80
aac gtc cag ctt gat cct gcg gct aac tta ggc atc gta aaa gtc gac			288
Asn Val Gln Leu Asp Pro Ala Ala Asn Leu Gly Ile Val Lys Val Asp			
85	90	95	
agc gac ggc gcg ggc tac cac att ctt tgg ggg tta acc aac gaa gcc			336
Ser Asp Gly Ala Gly Tyr His Ile Leu Trp Gly Leu Thr Asn Glu Ala			
100	105	110	
gtc ccc act tcc gaa ctt ccg gct cac ttc ctt tcc cac tgc gag cgc			384
Val Pro Thr Ser Glu Leu Pro Ala His Phe Leu Ser His Cys Glu Arg			
115	120	125	
att aaa gcc acc aac ggc aaa gat cgg gtg atc atg cac tgc cac gcc			432
Ile Lys Ala Thr Asn Gly Lys Asp Arg Val Ile Met His Cys His Ala			
130	135	140	
acc aac ctg atc gcc ctc acc tat gta ctt gaa aac gac acc gcg gtc			480
Thr Asn Leu Ile Ala Leu Thr Tyr Val Leu Glu Asn Asp Thr Ala Val			
145	150	155	160
ttc act cgc caa ctg tgg gaa ggc agc acc gag tgt ctg gtg gta ttc			528
Phe Thr Arg Gln Leu Trp Glu Gly Ser Thr Glu Cys Leu Val Val Phe			
165	170	175	
ccg gat ggc gtt ggc att ttg ccg tgg atg gtg ccc ggc acg gac gaa			576
Pro Asp Gly Val Gly Ile Leu Pro Trp Met Val Pro Gly Thr Asp Glu			
180	185	190	
atc ggc cag gcg acc gca caa gag atg caa aaa cat tcg ctg gtg ttg			624
Ile Gly Gln Ala Thr Ala Gln Glu Met Gln Lys His Ser Leu Val Leu			
195	200	205	
tgg ccc ttc cac ggc gtc ttc ggc agc gga ccg acg ctg gat gaa acc			672
Trp Pro Phe His Gly Val Phe Gly Ser Gly Pro Thr Leu Asp Glu Thr			
210	215	220	
ttc ggt tta atc gac acc gca gaa aaa tca gca caa gta tta gtg aag			720
Phe Gly Leu Ile Asp Thr Ala Glu Lys Ser Ala Gln Val Leu Val Lys			
225	230	235	240
gtt tat tcg atg ggc ggc atg aaa cag acc atc agc cgt gaa gag ttg			768
Val Tyr Ser Met Gly Gly Met Lys Gln Thr Ile Ser Arg Glu Glu Leu			
245	250	255	
ata gcg ctc ggc aag cgt ttc ggc gtt acg cca ctc gcc agt gcg ctg			816
Ile Ala Leu Gly Lys Arg Phe Gly Val Thr Pro Leu Ala Ser Ala Leu			
260	265	270	
gcg ctg taa			825
Ala Leu			

&lt;210&gt; 13

&lt;211&gt; 274

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 13

Met Gln Asn Ile Thr Gln Ser Trp Phe Val Gln Gly Met Ile Lys Ala			
1	5	10	15

Thr Thr Asp Ala Trp Leu Lys Gly Trp Asp Glu Arg Asn Gly Gly Asn			
20	25	30	

Leu Thr Leu Arg Leu Asp Asp Ala Asp Ile Ala Pro Tyr His Asp Asn		
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35	40	45
Phe His Gln Gln Pro Arg Tyr	Ile Pro Leu Ser Gln Pro Met Pro Leu	
50	55	60
Leu Ala Asn Thr Pro Phe Ile Val Thr Gly Ser Gly Lys Phe Phe Arg		
65	70	75
Asn Val Gln Leu Asp Pro Ala Ala Asn Leu Gly Ile Val Lys Val Asp		80
85	90	95
Ser Asp Gly Ala Gly Tyr His Ile Leu Trp Gly Leu Thr Asn Glu Ala		
100	105	110
Val Pro Thr Ser Glu Leu Pro Ala His Phe Leu Ser His Cys Glu Arg		
115	120	125
Ile Lys Ala Thr Asn Gly Lys Asp Arg Val Ile Met His Cys His Ala		
130	135	140
Thr Asn Leu Ile Ala Leu Thr Tyr Val Leu Glu Asn Asp Thr Ala Val		
145	150	155
Phe Thr Arg Gln Leu Trp Glu Gly Ser Thr Glu Cys Leu Val Val Phe		160
165	170	175
Pro Asp Gly Val Gly Ile Leu Pro Trp Met Val Pro Gly Thr Asp Glu		
180	185	190
Ile Gly Gln Ala Thr Ala Gln Glu Met Gln Lys His Ser Leu Val Leu		
195	200	205
Trp Pro Phe His Gly Val Phe Gly Ser Gly Pro Thr Leu Asp Glu Thr		
210	215	220
Phe Gly Leu Ile Asp Thr Ala Glu Lys Ser Ala Gln Val Leu Val Lys		
225	230	235
Val Tyr Ser Met Gly Gly Met Lys Gln Thr Ile Ser Arg Glu Glu Leu		240
245	250	255
Ile Ala Leu Gly Lys Arg Phe Gly Val Thr Pro Leu Ala Ser Ala Leu		
260	265	270
Ala Leu		

<210> 14  
<211> 939  
<212> DNA  
<213> Escherichia coli  
<220>  
<221> CDS  
<222> (1)..(936)  
<223> coding for rhaR (positive regulator for rhaRS operon)  
<400> 14

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Met Ala Phe Cys Asn Asn Ala Asn Leu Leu Asn Val Phe Val Arg His	
1 5 10 15	
att gcg aat aat caa ctt cgt tct ctg gcc gag gta gcc acg gtg gcg	96
Ile Ala Asn Asn Gln Leu Arg Ser Leu Ala Glu Val Ala Thr Val Ala	
20 25 30	
cat cag tta aaa ctt ctc aaa gat gat ttt ttt gcc agc gac cag cag	144
His Gln Leu Lys Leu Leu Lys Asp Asp Phe Phe Ala Ser Asp Gln Gln	
35 40 45	
gca gtc gct gtg gct gac cgt tat ccg caa gat gtc ttt gct gaa cat	192
Ala Val Ala Val Ala Asp Arg Tyr Pro Gln Asp Val Phe Ala Glu His	
50 55 60	
aca cat gat ttt tgt gag ctg gtg att gtc tgg cgc ggt aat ggc ctg	240
Thr His Asp Phe Cys Glu Leu Val Ile Val Trp Arg Gly Asn Gly Leu	
65 70 75 80	
cat gta ctc aac gat cgc cct tat cgc att acc cgt ggc gat ctc ttt	288

His Val Leu Asn Asp Arg Pro Tyr Arg Ile Thr Arg Gly Asp Leu Phe			
85	90	95	
tac att cat gct gac gat aaa cac tcc tac gct tcc gtt aac gat ctg			336
Tyr Ile His Ala Asp Asp Lys His Ser Tyr Ala Ser Val Asn Asp Leu			
100	105	110	
gtt ttg cag aat att att tat tgc ccg gag cgt ctg aag ctg aat ctt			384
Val Leu Gln Asn Ile Ile Tyr Cys Pro Glu Arg Leu Lys Leu Asn Leu			
115	120	125	
gac tgg cag ggg gcg att ccg gga ttt aac gcc agc gca ggg caa cca			432
Asp Trp Gln Gly Ala Ile Pro Gly Phe Asn Ala Ser Ala Gly Gln Pro			
130	135	140	
cac tgg cgc tta ggt agc atg ggg atg gcg cag gcg cggt atc			480
His Trp Arg Leu Gly Ser Met Gly Met Ala Gln Ala Arg Gln Val Ile			
145	150	155	160
ggt ctt gag cat gaa agt agt cag cat gtg ccg ttt gct aac gaa			528
Gly Gln Leu Glu His Glu Ser Ser Gln His Val Pro Phe Ala Asn Glu			
165	170	175	
atg gct gag ttg ctg ttc ggg cag ttg gtg atg ttg ctg aat cgc cat			576
Met Ala Glu Leu Leu Phe Gly Gln Leu Val Met Leu Leu Asn Arg His			
180	185	190	
cgt tac acc agt gat tcg ttg ccg cca aca tcc agc gaa acg ttg ctg			624
Arg Tyr Thr Ser Asp Ser Leu Pro Pro Thr Ser Ser Glu Thr Leu Leu			
195	200	205	
gat aag ctg att acc cgg ctg gcg gct agc ctg aaa agt ccc ttt gcg			672
Asp Lys Leu Ile Thr Arg Leu Ala Ala Ser Leu Lys Ser Pro Phe Ala			
210	215	220	
ctg gat aaa ttt tgt gat gag gca tcg tgc agt gag cgc gtt ttg cgt			720
Leu Asp Lys Phe Cys Asp Glu Ala Ser Cys Ser Glu Arg Val Leu Arg			
225	230	235	240
cag caa ttt cgc cag cag act gga atg acc atc aat caa tat ctg cga			768
Gln Gln Phe Arg Gln Gln Thr Gly Met Thr Ile Asn Gln Tyr Leu Arg			
245	250	255	
cag gtc aga gtg tgt cat gcg caa tat ctt ctc cag cat agc cgc ctg			816
Gln Val Arg Val Cys His Ala Gln Tyr Leu Leu Gln His Ser Arg Leu			
260	265	270	
tta atc agt gat att tcg acc gaa tgt ggc ttt gaa gat agt aac tat			864
Leu Ile Ser Asp Ile Ser Thr Glu Cys Gly Phe Glu Asp Ser Asn Tyr			
275	280	285	
ttt tcg gtg gtg ttt acc cgg gaa acc ggg atg acg ccc agc cag tgg			912
Phe Ser Val Val Phe Thr Arg Glu Thr Gly Met Thr Pro Ser Gln Trp			
290	295	300	
cgt cat ctc aat tcg cag aaa gat taa			939
Arg His Leu Asn Ser Gln Lys Asp			
305	310		

&lt;210&gt; 15

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 15

Met Ala Phe Cys Asn Asn Ala Asn Leu Leu Asn Val Phe Val Arg His

1 5 10 15

Ile Ala Asn Asn Gln Leu Arg Ser Leu Ala Glu Val Ala Thr Val Ala

20 25 30

His Gln Leu Lys Leu Leu Lys Asp Asp Phe Phe Ala Ser Asp Gln Gln

35 40 45

Ala Val Ala Val Ala Asp Arg Tyr Pro Gln Asp Val Phe Ala Glu His  
       50                  55                         60  
 Thr His Asp Phe Cys Glu Leu Val Ile Val Trp Arg Gly Asn Gly Leu  
       65                  70                  75                  80  
 His Val Leu Asn Asp Arg Pro Tyr Arg Ile Thr Arg Gly Asp Leu Phe  
       85                  90                         95  
 Tyr Ile His Ala Asp Asp Lys His Ser Tyr Ala Ser Val Asn Asp Leu  
       100                 105                         110  
 Val Leu Gln Asn Ile Ile Tyr Cys Pro Glu Arg Leu Lys Leu Asn Leu  
       115                 120                         125  
 Asp Trp Gln Gly Ala Ile Pro Gly Phe Asn Ala Ser Ala Gly Gln Pro  
       130                 135                         140  
 His Trp Arg Leu Gly Ser Met Gly Met Ala Gln Ala Arg Gln Val Ile  
       145                 150                         155                 160  
 Gly Gln Leu Glu His Glu Ser Ser Gln His Val Pro Phe Ala Asn Glu  
       165                 170                         175  
 Met Ala Glu Leu Leu Phe Gly Gln Leu Val Met Leu Leu Asn Arg His  
       180                 185                         190  
 Arg Tyr Thr Ser Asp Ser Leu Pro Pro Thr Ser Ser Glu Thr Leu Leu  
       195                 200                         205  
 Asp Lys Leu Ile Thr Arg Leu Ala Ala Ser Leu Lys Ser Pro Phe Ala  
       210                 215                         220  
 Leu Asp Lys Phe Cys Asp Glu Ala Ser Cys Ser Glu Arg Val Leu Arg  
       225                 230                         235                 240  
 Gln Gln Phe Arg Gln Gln Thr Gly Met Thr Ile Asn Gln Tyr Leu Arg  
       245                 250                         255  
 Gln Val Arg Val Cys His Ala Gln Tyr Leu Leu Gln His Ser Arg Leu  
       260                 265                         270  
 Leu Ile Ser Asp Ile Ser Thr Glu Cys Gly Phe Glu Asp Ser Asn Tyr  
       275                 280                         285  
 Phe Ser Val Val Phe Thr Arg Glu Thr Gly Met Thr Pro Ser Gln Trp  
       290                 295                         300  
 Arg His Leu Asn Ser Gln Lys Asp  
       305                 310

<210> 16  
 <211> 837  
 <212> DNA  
 <213> Escherichia coli  
 <220>  
 <221> CDS  
 <222> (1)...(834)  
 <223> coding for rhaS (positive regulator of rhaBAD operon)  
 <400> 16  
 atg acc gta tta cat agt gtg gat ttt ttt ccg tct ggt aac gcg tcc   48  
 Met Thr Val Leu His Ser Val Asp Phe Phe Pro Ser Gly Asn Ala Ser  
   1              5                 10                 15  
 gtg gcg ata gaa ccc cgg ctc ccg cag gcg gat ttt cct gaa cat cat   96  
 Val Ala Ile Glu Pro Arg Leu Pro Gln Ala Asp Phe Pro Glu His His  
   20              25                 30  
 cat gat ttt cat gaa att gtg att gtc gaa cat ggc acg ggt att cat   144  
 His Asp Phe His Glu Ile Val Ile Val Glu His Gly Thr Gly Ile His  
   35              40                 45  
 gtg ttt aat ggg cag ccc tat acc atc acc ggt ggc acg gtc tgt ttc   192  
 Val Phe Asn Gly Gln Pro Tyr Thr Ile Thr Gly Gly Thr Val Cys Phe  
   50              55                 60

gta	cgc	gat	cat	cat	gat	cg	cat	ctg	tat	gaa	cat	acc	gat	aat	ctg	tgt		240
Val	Arg	Asp	His	Asp	Arg	His	Leu	Tyr	Glu	His	Thr	Asp	Asn	Leu	Cys			
65							70		75								80	
ctg	acc	aat	gtg	ctg	tat	cgc	tcg	ccg	gat	cga	ttt	cag	ttt	ctc	gcc		288	
Leu	Thr	Asn	Val	Leu	Tyr	Arg	Ser	Pro	Asp	Arg	Phe	Gln	Phe	Leu	Ala			
							85		90							95		
ggg	ctg	aat	cag	ttg	ctg	cca	caa	gag	ctg	gat	ggg	cag	tat	ccg	tct		336	
Gly	Leu	Asn	Gln	Leu	Leu	Pro	Gln	Glu	Leu	Asp	Gly	Gln	Tyr	Pro	Ser			
							100		105							110		
cac	tgg	cgc	gtt	aac	cac	agc	gta	ttg	cag	cag	gtg	cga	cag	ctg	gtt		384	
His	Trp	Arg	Val	Asn	His	Ser	Val	Leu	Gln	Gln	Val	Arg	Gln	Leu	Val			
							115		120							125		
gca	cag	atg	gaa	cag	cag	gaa	ggg	gaa	aat	gat	tta	ccc	tcg	acc	gcc		432	
Ala	Gln	Met	Glu	Gln	Gln	Glu	Gly	Glu	Asn	Asp	Leu	Pro	Ser	Thr	Ala			
							130		135							140		
agt	cgc	gag	atc	ttg	ttt	atg	caa	tta	ctg	ctc	ttg	ctg	cgt	aaa	agc		480	
Ser	Arg	Glu	Ile	Leu	Phe	Met	Gln	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Lys	Ser		
							145		150							160		
agt	ttg	cag	gag	aac	ctg	gaa	aac	agc	gca	tca	cgt	ctc	aac	ttg	ctt		528	
Ser	Leu	Gln	Glu	Asn	Leu	Glu	Asn	Ser	Ala	Ser	Arg	Leu	Asn	Leu	Leu			
							165		170							175		
ctg	gcc	tgg	ctg	gag	gac	cat	ttt	gcc	gat	gag	gtg	aat	tgg	gat	gcc		576	
Leu	Ala	Trp	Leu	Glu	Asp	His	Phe	Ala	Asp	Glu	Val	Asn	Trp	Asp	Ala			
							180		185							190		
gtg	gcg	gat	caa	ttt	tct	ctt	tca	ctg	cgt	acg	cta	cat	cg	cag	ctt		624	
Val	Ala	Asp	Gln	Phe	Ser	Leu	Ser	Leu	Arg	Thr	Leu	His	Arg	Gln	Leu			
							195		200							205		
aag	cag	caa	acg	gga	ctg	acg	cct	cag	cga	tac	ctg	aac	cgc	ctg	cga		672	
Lys	Gln	Gln	Thr	Gly	Leu	Thr	Pro	Gln	Arg	Tyr	Leu	Asn	Arg	Leu	Arg			
							210		215							220		
ctg	atg	aaa	gcc	cga	cat	ctg	cta	cgc	cac	agc	gag	gcc	agc	gtt	act		720	
Leu	Met	Lys	Ala	Arg	His	Leu	Leu	Arg	His	Ser	Glu	Ala	Ser	Val	Thr			
							225		230							240		
gac	atc	gcc	tat	cgc	tgt	gga	ttc	agc	gac	agt	aac	cac	ttt	tcg	acg		768	
Asp	Ile	Ala	Tyr	Arg	Cys	Gly	Phe	Ser	Asp	Ser	Asn	His	Phe	Ser	Thr			
							245		250							255		
ctt	ttt	cgc	cga	gag	ttt	aac	tgg	tca	ccg	cgt	gat	att	cgc	cag	gga		816	
Leu	Phe	Arg	Arg	Glu	Phe	Asn	Trp	Ser	Pro	Arg	Asp	Ile	Arg	Gln	Gly			
							260		265							270		
cg	gat	ggc	ttt	ctg	caa	taa											837	
Arg	Asp	Gly	Phe	Leu	Gln													
						275												

&lt;210&gt; 17

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 17

Met Thr Val Leu His Ser Val Asp Phe Phe Pro Ser Gly Asn Ala Ser

1 5 10 15

Val Ala Ile Glu Pro Arg Leu Pro Gln Ala Asp Phe Pro Glu His His

20 25 30

His Asp Phe His Glu Ile Val Ile Val Glu His Gly Thr Gly Ile His

35 40 45

Val Phe Asn Gly Gln Pro Tyr Thr Ile Thr Gly Gly Thr Val Cys Phe

50 55 60

Val Arg Asp His Asp Arg His Leu Tyr Glu His Thr Asp Asn Leu Cys  
 65 70 75 80  
 Leu Thr Asn Val Leu Tyr Arg Ser Pro Asp Arg Phe Gln Phe Leu Ala  
 85 90 95  
 Gly Leu Asn Gln Leu Leu Pro Gln Glu Leu Asp Gly Gln Tyr Pro Ser  
 100 105 110  
 His Trp Arg Val Asn His Ser Val Leu Gln Gln Val Arg Gln Leu Val  
 115 120 125  
 Ala Gln Met Glu Gln Gln Glu Gly Glu Asn Asp Leu Pro Ser Thr Ala  
 130 135 140  
 Ser Arg Glu Ile Leu Phe Met Gln Leu Leu Leu Leu Arg Lys Ser  
 145 150 155 160  
 Ser Leu Gln Glu Asn Leu Glu Asn Ser Ala Ser Arg Leu Asn Leu Leu  
 165 170 175  
 Leu Ala Trp Leu Glu Asp His Phe Ala Asp Glu Val Asn Trp Asp Ala  
 180 185 190  
 Val Ala Asp Gln Phe Ser Leu Ser Leu Arg Thr Leu His Arg Gln Leu  
 195 200 205  
 Lys Gln Gln Thr Gly Leu Thr Pro Gln Arg Tyr Leu Asn Arg Leu Arg  
 210 215 220  
 Leu Met Lys Ala Arg His Leu Leu Arg His Ser Glu Ala Ser Val Thr  
 225 230 235 240  
 Asp Ile Ala Tyr Arg Cys Gly Phe Ser Asp Ser Asn His Phe Ser Thr  
 245 250 255  
 Leu Phe Arg Arg Glu Phe Asn Trp Ser Pro Arg Asp Ile Arg Gln Gly  
 260 265 270  
 Arg Asp Gly Phe Leu Gln  
 275

<210> 18  
 <211> 1035  
 <212> DNA  
 <213> Escherichia coli  
 <220>  
 <221> CDS  
 <222> (1)..(1032)  
 <223> coding for rhaT (rhamnose transport protein)  
 <400> 18

atg	agt	aac	gca	att	acg	atg	ggg	ata	ttt	tgg	cat	ttg	atc	ggc	gca	48
Met	Ser	Asn	Ala	Ile	Thr	Met	Gly	Ile	Phe	Trp	His	Leu	Ile	Gly	Ala	
1				5				10					15			
gcc	agt	gca	gcc	tgt	ttt	tac	gct	ccg	ttc	aaa	aaa	gta	aaa	aaa	tgg	96
Ala	Ser	Ala	Ala	Cys	Phe	Tyr	Ala	Pro	Phe	Lys	Lys	Val	Lys	Lys	Trp	
20				25								30				
tca	tgg	gaa	acc	atg	tgg	tca	gtc	ggt	ggg	att	gtt	tcg	tgg	att	att	144
Ser	Trp	Glu	Thr	Met	Trp	Ser	Val	Gly	Gly	Ile	Val	Ser	Trp	Ile	Ile	
35				40							45					
ctg	ccg	tgg	gcc	atc	agc	gcc	ctg	tta	cta	ccg	aat	ttc	tgg	gca	tat	192
Leu	Pro	Trp	Ala	Ile	Ser	Ala	Leu	Leu	Leu	Pro	Asn	Phe	Trp	Ala	Tyr	
50				55							60					
tac	agc	tcg	ttt	agt	ctc	tct	acg	cga	ctg	cct	gtt	ttt	ctg	ttc	ggc	240
Tyr	Ser	Ser	Phe	Ser	Leu	Ser	Thr	Arg	Leu	Pro	Val	Phe	Leu	Phe	Gly	
65			70					75			80					
gct	atg	tgg	ggg	atc	ggt	aat	atc	aac	tac	ggc	ctg	acc	atg	cgt	tat	288
Ala	Met	Trp	Gly	Ile	Gly	Asn	Ile	Asn	Tyr	Gly	Leu	Thr	Met	Arg	Tyr	
85				90							95					

ctc ggc atg tcg atg gga att ggc atc gcc att ggc att acg ttg att	336
Leu Gly Met Ser Met Gly Ile Gly Ile Ala Ile Gly Ile Thr Leu Ile	
100 105 110	
gtc ggt acg ctg atg acg cca att atc aac ggc aat ttc gat gtg ttg	384
Val Gly Thr Leu Met Thr Pro Ile Ile Asn Gly Asn Phe Asp Val Leu	
115 120 125	
att agc acc gaa ggc gga cgc atg acg ttg ctc ggc gtt ctg gtg gcg	432
Ile Ser Thr Glu Gly Gly Arg Met Thr Leu Leu Gly Val Leu Val Ala	
130 135 140	
ctg att ggc gta ggg att gta act cgc gcc ggg cag ttg aaa gag cgc	480
Leu Ile Gly Val Gly Ile Val Thr Arg Ala Gly Gln Leu Lys Glu Arg	
145 150 155 160	
aag atg ggc att aaa gcc gaa gag ttc aat ctg aaa aaa ggg ctg gtg	528
Lys Met Gly Ile Lys Ala Glu Glu Phe Asn Leu Lys Lys Gly Leu Val	
165 170 175	
ctg gcg gtg atg tgc ggc att ttc tct gcc ggg atg tcc ttt gcg atg	576
Leu Ala Val Met Cys Gly Ile Phe Ser Ala Gly Met Ser Phe Ala Met	
180 185 190	
aac gcc gca aaa ccg atg cat gaa gcc gct gcc gca ctt ggc gtc gat	624
Asn Ala Ala Lys Pro Met His Glu Ala Ala Ala Leu Gly Val Asp	
195 200 205	
cca ctg tat gtc gct ctg cca agc tat gtt gtc atc atg ggc ggc ggc	672
Pro Leu Tyr Val Ala Leu Pro Ser Tyr Val Val Ile Met Gly Gly Gly	
210 215 220	
gcg atc att aac ctc ggt ttc tgt ttt att cgt ctg gca aaa gtg aag	720
Ala Ile Ile Asn Leu Gly Phe Cys Phe Ile Arg Leu Ala Lys Val Lys	
225 230 235 240	
gat ttg tcg cta aaa gcc gac ttc tcg ctg gca aaa tcg ctg atc att	768
Asp Leu Ser Leu Lys Ala Asp Phe Ser Leu Ala Lys Ser Leu Ile Ile	
245 250 255	
cac aat gtg tta ctc tcg aca ctg ggc ggg ttg atg tgg tat ctg caa	816
His Asn Val Leu Leu Ser Thr Leu Gly Gly Leu Met Trp Tyr Leu Gln	
260 265 270	
ttc ttt ttc tat gcc tgg ggc cac gcc cgc att ccg gcg cag tat gac	864
Phe Phe Phe Tyr Ala Trp Gly His Ala Arg Ile Pro Ala Gln Tyr Asp	
275 280 285	
tac atc agt tgg atg ctg cat atg agt ttc tat gta ttg tgc ggc ggt	912
Tyr Ile Ser Trp Met Leu His Met Ser Phe Tyr Val Leu Cys Gly Gly	
290 295 300	
atc gtc ggg ctg gtg ctg aaa gag tgg aac aat gca gga cgc cgt ccg	960
Ile Val Gly Leu Val Leu Lys Glu Trp Asn Asn Ala Gly Arg Arg Pro	
305 310 315 320	
gta acg gtg ttg agc ctc ggt tgt gtg att att gtc gcc gct aac	1008
Val Thr Val Leu Ser Leu Gly Cys Val Val Ile Ile Val Ala Ala Asn	
325 330 335	
atc gtc ggc atc ggc atg gcg aat taa	1035
Ile Val Gly Ile Gly Met Ala Asn	
340	

&lt;210&gt; 19

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 19

Met Ser Asn Ala Ile Thr Met Gly Ile Phe Trp His Leu Ile Gly Ala

1

5

10

15

Ala Ser Ala Ala Cys Phe Tyr Ala Pro Phe Lys Lys Val Lys Lys Trp  
     20                     25                     30  
 Ser Trp Glu Thr Met Trp Ser Val Gly Gly Ile Val Ser Trp Ile Ile  
     35                     40                     45  
 Leu Pro Trp Ala Ile Ser Ala Leu Leu Leu Pro Asn Phe Trp Ala Tyr  
     50                     55                     60  
 Tyr Ser Ser Phe Ser Leu Ser Thr Arg Leu Pro Val Phe Leu Phe Gly  
     65                     70                     75                     80  
 Ala Met Trp Gly Ile Gly Asn Ile Asn Tyr Gly Leu Thr Met Arg Tyr  
     85                     90                     95  
 Leu Gly Met Ser Met Gly Ile Gly Ile Ala Ile Gly Ile Thr Leu Ile  
    100                     105                     110  
 Val Gly Thr Leu Met Thr Pro Ile Ile Asn Gly Asn Phe Asp Val Leu  
    115                     120                     125  
 Ile Ser Thr Glu Gly Gly Arg Met Thr Leu Leu Gly Val Leu Val Ala  
    130                     135                     140  
 Leu Ile Gly Val Gly Ile Val Thr Arg Ala Gly Gln Leu Lys Glu Arg  
    145                     150                     155                     160  
 Lys Met Gly Ile Lys Ala Glu Glu Phe Asn Leu Lys Lys Gly Leu Val  
    165                     170                     175  
 Leu Ala Val Met Cys Gly Ile Phe Ser Ala Gly Met Ser Phe Ala Met  
    180                     185                     190  
 Asn Ala Ala Lys Pro Met His Glu Ala Ala Ala Leu Gly Val Asp  
    195                     200                     205  
 Pro Leu Tyr Val Ala Leu Pro Ser Tyr Val Val Ile Met Gly Gly Gly  
    210                     215                     220  
 Ala Ile Ile Asn Leu Gly Phe Cys Phe Ile Arg Leu Ala Lys Val Lys  
    225                     230                     235                     240  
 Asp Leu Ser Leu Lys Ala Asp Phe Ser Leu Ala Lys Ser Leu Ile Ile  
    245                     250                     255  
 His Asn Val Leu Leu Ser Thr Leu Gly Gly Leu Met Trp Tyr Leu Gln  
    260                     265                     270  
 Phe Phe Phe Tyr Ala Trp Gly His Ala Arg Ile Pro Ala Gln Tyr Asp  
    275                     280                     285  
 Tyr Ile Ser Trp Met Leu His Met Ser Phe Tyr Val Leu Cys Gly Gly  
    290                     295                     300  
 Ile Val Gly Leu Val Leu Lys Glu Trp Asn Asn Ala Gly Arg Arg Pro  
    305                     310                     315                     320  
 Val Thr Val Leu Ser Leu Gly Cys Val Val Ile Ile Val Ala Ala Asn  
    325                     330                     335  
 Ile Val Gly Ile Gly Met Ala Asn  
    340